AMENDMENTS TO THE CLAIMS

Claim 1 (Currently Amended): A method of differentiating bottom-fermenting yeast from wild yeast comprising

synthesizing a pair of primers consisting of (i) a primer consisting of the base sequence set forth in SEQ ID NO: 7 and (ii) a primer consisting of 15-30 nucleotides of a sequence that is complementary to a base sequence of chromosome IX of *Saccharomyces cerevisiae* located downstream from a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 6;

performing PCR (Polymerase Chain Reaction) to produce a PCR amplification product, wherein the primers for said PCR consist of said pair of primers, the template for said PCR is a DNA separated from a yeast specimen, and said PCR is performed by denaturing for 10 seconds to 2 minutes at a temperature of 90-98°C, annealing for 20 seconds to 2 minutes at a temperature of 40-75°C, and extending for 1-20 minutes at a temperature of 65-75°C, with 10-30 cycles; and

differentiating whether said yeast is bottom-fermenting yeast or wild yeast, based on the PCR amplification product,

wherein said wild yeast is yeast not used for brewing and ~~being obtained from~~ said wild yeast belongs to a genus selected from the group consisting of the genus *Hansenula*, the genus *Brettanomyces*, the genus *Candida*, and the genus *Saccharomyces*, wherein when the wild yeast is from the genus *Saccharmyces* said wild yeast is a species selected from the group consisting of *Saccharomyces cerevisiae*, *Saccharomyces bayanus* and *Saccharomyces diastaticus*, and

wherein said bottom-fermenting yeast is *Saccharomyces pastorianus*.

Claim 2 (Currently Amended): A method of differentiating bottom-fermenting yeast from wild yeast comprising

synthesizing a pair of primers consisting of (i) a primer consisting of the base sequence set forth in SEQ ID NO: 7 and (ii) a primer consisting of the base sequence set forth in SEQ ID NO: 8;

performing PCR (Polymerase Chain Reaction) to produce a PCR amplification product, wherein the primers for said PCR consist of said pair of primers, the template for said PCR is a DNA separated from a yeast specimen, and said PCR is performed by denaturing for 10 seconds to 2 minutes at a temperature of 90-98°C, annealing for 20 seconds to 2 minutes at a temperature of 40-75°C, and extending for 1-20 minutes at a temperature of 65-75°C, with 10-30 cycles; and

differentiating whether said yeast is bottom-fermenting yeast or wild yeast, based on the PCR amplification product,

wherein said wild yeast is yeast not used for brewing and ~~being obtained from~~ said wild yeast belongs to a genus selected from the group consisting of the genus *Hansenula*, the genus *Brettanomyces*, the genus *Candida*, and the genus *Saccharomyces*, wherein when the wild yeast is from the genus *Saccharmyces* said wild yeast is a species selected from the group consisting of *Saccharomyces cerevisiae*, *Saccharomyces bayanus* and *Saccharomyces diastaticus*, and

wherein said bottom-fermenting yeast is *Saccharomyces pastorianus*.

Claim 3 (Canceled):

Claim 4 (Currently Amended): A method of differentiating beer yeast comprising

synthesizing a pair of primers consisting of (i) a primer consisting of the base sequence set forth in SEQ ID NO: 9 and (ii) a primer consisting of 15-30 bp of a sequence that is complementary to a base sequence of chromosome IX of *Saccharomyces cerevisiae* located downstream from a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 6;

performing PCR (Polymerase Chain Reaction) to produce a PCR amplification product, wherein the primers for said PCR consist of said pair of primers, the template for said PCR is a DNA separated from a yeast specimen, and said PCR is performed by denaturing for 10 seconds to 2 minutes at a temperature of 90-98°C, annealing for 20 seconds to 2 minutes at a temperature of 40-75°C, and extending for 1-20 minutes at a temperature of 65-75°C, with 10-30 cycles; and

differentiating whether said yeast is bottom-fermenting yeast or wild yeast, based on the PCR amplification product,

wherein said wild yeast is yeast not used for brewing and ~~being obtained from~~ said wild yeast belongs to a genus selected from the group consisting of the genus *Hansenula*, the genus *Brettanomyces*, the genus *Candida*, and the genus *Saccharomyces*, wherein when the wild yeast is from the genus *Saccharmyces* said wild yeast is a species selected from the group consisting of *Saccharomyces cerevisiae*, *Saccharomyces bayanus* and *Saccharomyces diastaticus*, and

wherein said bottom-fermenting yeast is *Saccharomyces pastorianus*.

Claim 5 (Withdrawn): The method of differentiating beer yeast according to claim 4, wherein said pair of primers consists of (i) a primer comprising the base sequence set forth in SEQ ID NO: 9 and (ii) a primer comprising the base sequence set forth in SEQ ID NO: 10.

Claim 6 (Withdrawn): The method of differentiating beer yeast according to claim 5, wherein the base sequences of said primers have one or more base substitutions, deletions or insertions and function as primers for PCR.

Claim 7 (Previously Presented): A pair of primers consisting of (i) a primer consisting of the base sequence set forth in SEQ ID NO: 7 and (ii) a primer consisting of the base sequence set forth in SEQ ID NO: 8.

Claim 8 (Canceled)

Claim 9 (Withdrawn): A pair of primers consisting of (i) a primer comprising the base sequence set forth in SEQ ID NO: 9 and (ii) a primer comprising the base sequence set forth in SEQ ID NO: 10.

Claim 10 (Withdrawn): The pair of primers according to claim 9, wherein the base sequences of said primers have one or more base substitutions, deletions or insertions and function as primers for PCR.